Due to the comparison of the similar datasets ID, SD1, SD2, SD3 an observer can make a more profound assessment of the risk or clinical significance. Thus, the interobserver variability can be reduced by the inventive method.

[0103] FIG. **3** shows a block diagram of a first embodiment IIIa of act III of the inventive method.

[0104] In act ia, a case dataset is provided as input data which includes a PI-RADS value, lesion size and/or lesion location as radiological data. A radiologist can evaluate these radiological parameters in advance. Alternatively, lesion size and/or lesion location can be obtained via a CAD algorithm. In addition, the input data includes information of the EHR, such as PSA value, PSA density, patient age.

[0105] In act iia, the inputs are normalized. For example, the lesion size can be adjusted to the patient size or the like.

[0106] In act iiia, the inputs are evaluated be the method. The AI-based method can be designed, for example, as a simple machine learning method such as e.g. an SVM method.

[0107] In act iva, the output of the definitive feature DF is obtained in the form of a simple scalar value describing the risk factor of the case dataset.

[0108] The AI-based method of IIIa is trained with a fixed number of defined input variables and by minimizing the difference of the obtained risk factor to the histological assessed Gleason score, which serves as ground truth.

[0109] The same input variables as during the training are used for real application of the method after training.

[0110] In this embodiment, the distance measure for comparing the similarity of different case datasets is simply the difference between the respective risk factors which are obtained as definitive features DF.

[0111] FIG. **4** shows a block diagram of a second embodiment IIIb of act III of the inventive method.

[0112] In act ib, a case dataset is provided as input data which includes an mpMR image.

[0113] In act iib, a region of interest is identified in the mpMR image and the image is segmented. This can be achieved by applying a CAD algorithm or a machine learning method trained for the purpose of lesion detection and segmentation.

[0114] In act iiib, the actual AI-based method evaluates the definitive features DF by extracting generic radiomic features from the mpMR images and a correlation analysis to select from the redundant features.

[0115] In act ivb, a vector of the (scalar) selected radiomic features is output as definitive feature DF.

[0116] The AI-based method of IIIb is trained using a ROC-Curve analysis with the histologically determined Gleason score as ground truth, wherein the extracted radiomic features can directly be used to distinguish between different Gleason score groups. The AI-based method may be designed as a random forest method. For example, cases with Gleason score (GS) larger than 6 can be considered as positive class (malignant) and GS<=6 belong to a negative class (benign). Then a binary classifier can be implemented to discriminate the two classes. Moreover, an ordinal classification can be performed, in which the probability of being each GS category, e.g. GS<=6, GS=7, GS=8, and GS>=9 can be predicted.

[0117] FIG. **5** shows a block diagram of a third embodiment IIIc of act III of the inventive method.

[0118] In act ic, a case dataset is provided as input data which includes an mpMR image.

[0119] In act iic, a region of interest is identified in the mpMR image and the image is segmented. This can be achieved by applying a CAD algorithm or a machine learning method trained for the purpose of lesion detection and segmentation.

[0120] In act iiic, the actual AI-based method is implemented as a decoder network with respect to decoded, abstract (non-generic) features.

[0121] In act ivc, a risk value in form of a predicted gleason score is obtained from the decoded features by a classification network as a first component of the definitive feature.

[0122] In act vc, standard radiomic features as well as a PI-RADS value are obtained from the decoded features by a decoder network as a lesion-specific fingerprint.

[0123] The lesion-specific fingerprint is used as further constraint to the otherwise under defined problem, to keep the physical properties of the lesion close to the PI-RADS.

[0124] The risk value and the lesion-specific fingerprint are output as definitive features.

[0125] The AI-based method of IIIc is trained using a ROC-Curve analysis by comparing the risk factor predicted by the AI-decoder-classification network with the histologically determined Gleason score as ground truth.

[0126] FIG. **6** shows a block diagram of a fourth embodiment IIId of act III of the inventive method.

[0127] Here, two subnetworks are used for the evaluation.

[0128] In act id, a first part of the case dataset, which includes an mpMR image, is provided as input data for the first subnetwork.

[0129] In act iid, a second part of the case dataset, which includes additional parameters from the EHR (as described above), is provided as input data for the second subnetwork.

[0130] In act iid, a region of interest is identified in the mpMR image and the image is segmented. This can be achieved by applying a CAD algorithm or a machine learning method trained for the purpose of lesion detection and segmentation.

[0131] In act iiid, the first subnetwork, which is designed as convolutional neural network (CNN), extracts features from the mpMR image. The convolutional neural network may be of the type of a ResNet or DenseNet.

[0132] In act ivd, the second subnetwork, which is designed as fully connected network, extracts features from the additional parameters.

[0133] In act vd, the extracted parameters of the first subnetwork and the second subnetwork are integrated into a vector which is output includes the definitive features DF as components.

[0134] The AI-based method of IIIc is trained by minimizing a triplet loss function L of the form

$$L(A,P,N)=\max(D(A,P)-D(A,N)+\alpha,0) \quad \text{Eq. 4,}$$

wherein A is the anchor lesion (reference), P is the positive example (lesion with the same histological result), and N is the negative example (lesion with different histological result). D is one of the above mentioned distance measures. Thus, the network that makes the distance between the encoding features of the anchor and positive example to be less than or equal to the distance between the encoding features of the anchor and negative example is promoted. The ground truth of the histological information is built on biopsy results. Two lesions with the same Gleason score are positive examples to each other.